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SEQUENCE LISTING

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SANDRIN, MAURO SERGIO

<120> IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
GLYCOSYLTRANSFERASE

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<141> 1998-03-31

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<151> 1997-08-01

<150> 60/024,279

<151> 1996-08-21

<150> P01402

<151> 1996-08-02

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1043

<212> DNA

<213> Sus Domesticus

<220>

<221> CDS

<222> (9)..(1031)

<400> 1

ctacagcc atg ctc agc atg cag gca tcc ttc ttc ccc acg ggt ccc 50

Met Leu Ser Met Gln Ala Ser Phe Phe Phe Pro Thr Gly Pro

1

5

10

ttc atc ctc ttt gtc ttc acg gct tcc acc ata ttt cac ctt cag cag

Phe Ile Leu Phe Val Phe Thr Ala Ser Thr Ile Phe His Leu Gln Gln

15

20

25

98

agg atg gtg aag att caa ccc acg tgg gag tta cag atg gtg acg cag

Arg Met Val Lys Ile Gln Pro Thr Trp Glu Leu Gln Met Val Thr Gln

35

40

45

146

gtg acc aca gag agc ccc tcg agc ccc cag ctg aag ggc atg tgg acg	194		
Val Thr Thr Glu Ser Pro Ser Ser Pro Gln Leu Lys Gly Met Trp Thr			
50	55	60	
atc aat gcc atc ggc cgc ctg ggg aac cag atg ggg gag tac gcc acc	242		
Ile Asn Ala Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr			
65	70	75	
ctg tac gcg ctg gcc agg atg aac ggg cgg ccg gcc ttc atc ccg ccc	290		
Leu Tyr Ala Leu Ala Arg Met Asn Gly Arg Pro Ala Phe Ile Pro Pro			
80	85	90	
gag atg cac agc acg ctg gcc ccc atc ttc agg atc acc ctc ccg gtc	338		
Glu Met His Ser Thr Leu Ala Pro Ile Phe Arg Ile Thr Leu Pro Val			
95	100	105	110
ctg cac gcc agc acg gcc cgc agg atc ccc tgg cag aac tac cac ctg	386		
Leu His Ala Ser Thr Ala Arg Arg Ile Pro Trp Gln Asn Tyr His Leu			
115	120	125	
aac gac tgg atg gag gag cgg tac cgc cac atc ccg ggg gag tac gtg	434		
Asn Asp Trp Met Glu Glu Arg Tyr Arg His Ile Pro Gly Glu Tyr Val			
130	135	140	
cgc ctc acg ggc tac ccc tgc tcc tgg acc ttc tac cac cac ctg cgc	482		
Arg Leu Thr Gly Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg			
145	150	155	
acc gag atc ctc cgg gag ttc acc ctg cat aac cac gtg cgc gag gag	530		
Thr Glu Ile Leu Arg Glu Phe Thr Leu His Asn His Val Arg Glu Glu			
160	165	170	
gcc cag gat ttc ctg cgg ggt ctg cgg gtg aac ggg agc cga ccg agt	578		
Ala Gln Asp Phe Leu Arg Gly Leu Arg Val Asn Gly Ser Arg Pro Ser			
175	180	185	190
acc tac gtg ggg gtg cac gtg cgc cgg ggg gac tac gtg cac gtg atg	626		
Thr Tyr Val Gly Val His Val Arg Arg Gly Asp Tyr Val His Val Met			
195	200	205	
ccc aac gtg tgg aag ggc gtg gtg gcc gac cgg cgg tac ctg gag cag	674		
Pro Asn Val Trp Lys Gly Val Val Ala Asp Arg Arg Tyr Leu Glu Gln			
210	215	220	
gcc ctg gac tgg ttc cgg gct cgc tac cgc tcc ccc gtc ttt gtg gtc	722		
Ala Leu Asp Trp Phe Arg Ala Arg Tyr Arg Ser Pro Val Phe Val Val			
225	230	235	

tcc agc aac ggc atg gcc tgg tgt cgg gaa aac atc aat gcc tcg cgc	770		
Ser Ser Asn Gly Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg			
240	245	250	
ggc gat gtg gtg ttt gcc ggc aat ggc atc gag ggc tcc ccc gcc aaa	818		
Gly Asp Val Val Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys			
255	260	265	270
gac ttc gcg ctg ctc acg cag tgt aac cac act gtc atg acc att ggc	866		
Asp Phe Ala Leu Leu Thr Gln Cys Asn His Thr Val Met Thr Ile Gly			
275	280	285	
acg ttc ggg atc tgg gcc gcc tac ctt gct ggt gga gag acc atc tac	914		
Thr Phe Gly Ile Trp Ala Ala Tyr Leu Ala Gly Gly Glu Thr Ile Tyr			
290	295	300	
ctg gcc aat tac acg ctc ccg gac tct ccc ttc ctc aaa ctc ttt aag	962		
Leu Ala Asn Tyr Thr Leu Pro Asp Ser Pro Phe Leu Lys Leu Phe Lys			
305	310	315	
ccc gag gca gcc ttc ctg ccc gag tgg att ggg atc gag gca gac ctg	1010		
Pro Glu Ala Ala Phe Leu Pro Glu Trp Ile Gly Ile Glu Ala Asp Leu			
320	325	330	
tcc cca ctc ctt aag cac tga tgtcggctgt cc	1043		
Ser Pro Leu Leu Lys His			
335	340		

<210> 2
 <211> 340
 <212> PRT
 <213> Sus Domesticus

<400> 2
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 20 25 30
 Val Lys Ile Gln Pro Thr Trp Glu Leu Gln Met Val Thr Gln Val Thr
 35 40 45
 Thr Glu Ser Pro Ser Pro Gln Leu Lys Gly Met Trp Thr Ile Asn
 50 55 60
 Ala Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Tyr
 65 70 75 80
 Ala Leu Ala Arg Met Asn Gly Arg Pro Ala Phe Ile Pro Pro Glu Met
 85 90 95
 His Ser Thr Leu Ala Pro Ile Phe Arg Ile Thr Leu Pro Val Leu His

100	105	110
Ala Ser Thr Ala Arg Arg Ile Pro Trp Gln Asn Tyr His Leu Asn Asp		
115	120	125
Trp Met Glu Glu Arg Tyr Arg His Ile Pro Gly Glu Tyr Val Arg Leu		
130	135	140
Thr Gly Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg Thr Glu		
145	150	155
Ile Leu Arg Glu Phe Thr Leu His Asn His Val Arg Glu Glu Ala Gln		
165	170	175
Asp Phe Leu Arg Gly Leu Arg Val Asn Gly Ser Arg Pro Ser Thr Tyr		
180	185	190
Val Gly Val His Val Arg Arg Gly Asp Tyr Val His Val Met Pro Asn		
195	200	205
Val Trp Lys Gly Val Val Ala Asp Arg Arg Tyr Leu Glu Gln Ala Leu		
210	215	220
Asp Trp Phe Arg Ala Arg Tyr Arg Ser Pro Val Phe Val Val Ser Ser		
225	230	235
Asn Gly Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg Gly Asp		
245	250	255
Val Val Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys Asp Phe		
260	265	270
Ala Leu Leu Thr Gln Cys Asn His Thr Val Met Thr Ile Gly Thr Phe		
275	280	285
Gly Ile Trp Ala Ala Tyr Leu Ala Gly Gly Glu Thr Ile Tyr Leu Ala		
290	295	300
Asn Tyr Thr Leu Pro Asp Ser Pro Phe Leu Lys Leu Phe Lys Pro Glu		
305	310	315
Ala Ala Phe Leu Pro Glu Trp Ile Gly Ile Glu Ala Asp Leu Ser Pro		
325	330	335
Leu Leu Lys His		
340		

<210> 3
 <211> 1098
 <212> DNA
 <213> Sus Domesticus

<220>
 <221> CDS
 <222> (1)..(1098)

<400> 3
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 Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu Leu Val
 1 5 10 15

tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac ctc ttt			96
Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe			
20	25	30	
tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac gtg gta			144
Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val			
35	40	45	
tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta cac ccc			192
Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro			
50	55	60	
aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc ggg acc			240
Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr			
65	70	75	80
tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga cag tat			288
Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr			
85	90	95	
gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc ttc atc			336
Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile			
100	105	110	
cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc acg ctg			384
Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu			
115	120	125	
cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg gag ctg			432
Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu			
130	135	140	
gag ctt cac gac tgg atg tcc gag gat tat gcc cac tta aag gag ccc			480
Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro			
145	150	155	160
tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc cac cac			528
Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His			
165	170	175	
ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac ctt cgg			576
Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg			
180	185	190	
caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc aca ggg			624
Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly			
195	200	205	

gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg gac tat	672		
Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr			
210	215	220	
ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac ggc gct	720		
Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Ala			
225	230	235	240
tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa gcc ccc	768		
Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro			
245	250	255	
gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag aac atc	816		
Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile			
260	265	270	
gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg gag gcc	864		
Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala			
275	280	285	
gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac acc atc	912		
Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile			
290	295	300	
atg acc att ggc acc ttc ggc ttc tgg gcc tac ctg gct ggt gga	960		
Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly			
305	310	315	320
gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc ttc ctg	1008		
Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu			
325	330	335	
aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg ggc att	1056		
Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile			
340	345	350	
aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct tga	1098		
Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro			
355	360	365	

<210> 4
 <211> 365
 <212> PRT
 <213> Sus Domesticus

<400> 4
 Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu Leu Val

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					20			25						30	
Tyr	Ser	Gly	Leu	Asp	Leu	Leu	Ala	Leu	Cys	Pro	Asp	His	Asn	Val	Val
					35			40					45		
Ser	Ser	Pro	Val	Ala	Ile	Phe	Cys	Leu	Ala	Gly	Thr	Pro	Val	His	Pro
					50			55					60		
Asn	Ala	Ser	Asp	Ser	Cys	Pro	Lys	His	Pro	Ala	Ser	Phe	Ser	Gly	Thr
					65			70					75		80
Trp	Thr	Ile	Tyr	Pro	Asp	Gly	Arg	Phe	Gly	Asn	Gln	Met	Gly	Gln	Tyr
					85			90					95		
Ala	Thr	Leu	Leu	Ala	Leu	Ala	Gln	Leu	Asn	Gly	Arg	Gln	Ala	Phe	Ile
					100			105					110		
Gln	Pro	Ala	Met	His	Ala	Val	Leu	Ala	Pro	Val	Phe	Arg	Ile	Thr	Leu
					115			120					125		
Pro	Val	Leu	Ala	Pro	Glu	Val	Asp	Arg	His	Ala	Pro	Trp	Arg	Glu	Leu
					130			135					140		
Glu	Leu	His	Asp	Trp	Met	Ser	Glu	Asp	Tyr	Ala	His	Leu	Lys	Glu	Pro
					145			150					155		160
Trp	Leu	Lys	Leu	Thr	Gly	Phe	Pro	Cys	Ser	Trp	Thr	Phe	Phe	His	His
					165			170					175		
Leu	Arg	Glu	Gln	Ile	Arg	Ser	Glu	Phe	Thr	Leu	His	Asp	His	Leu	Arg
					180			185					190		
Gln	Glu	Ala	Gln	Gly	Val	Leu	Ser	Gln	Phe	Arg	Leu	Pro	Arg	Thr	Gly
					195			200					205		
Asp	Arg	Pro	Ser	Thr	Phe	Val	Gly	Val	His	Val	Arg	Arg	Gly	Asp	Tyr
					210			215					220		
Leu	Arg	Val	Met	Pro	Lys	Arg	Trp	Lys	Gly	Val	Val	Gly	Asp	Gly	Ala
					225			230					235		240
Tyr	Leu	Gln	Gln	Ala	Met	Asp	Trp	Phe	Arg	Ala	Arg	Tyr	Glu	Ala	Pro
					245			250					255		
Val	Phe	Val	Val	Thr	Ser	Asn	Gly	Met	Glu	Trp	Cys	Arg	Lys	Asn	Ile
					260			265					270		
Asp	Thr	Ser	Arg	Gly	Asp	Val	Ile	Phe	Ala	Gly	Asp	Gly	Arg	Glu	Ala
					275			280					285		
Ala	Pro	Ala	Arg	Asp	Phe	Ala	Leu	Leu	Val	Gln	Cys	Asn	His	Thr	Ile
					290			295					300		
Met	Thr	Ile	Gly	Thr	Phe	Gly	Phe	Trp	Ala	Ala	Tyr	Leu	Ala	Gly	Gly
					305			310					315		320
Asp	Thr	Ile	Tyr	Leu	Ala	Asn	Phe	Thr	Leu	Pro	Thr	Ser	Ser	Phe	Leu
					325			330					335		
Lys	Ile	Phe	Lys	Pro	Glu	Ala	Ala	Phe	Leu	Pro	Glu	Trp	Val	Gly	Ile
					340			345					350		
Asn	Ala	Asp	Leu	Ser	Pro	Leu	Gln	Met	Leu	Ala	Gly	Pro			
					355			360					365		

<210> 5
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 5
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<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 6
gctctagagc gtcagatgtt atttctaacc aaattatac 39

<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 7
gcggatccat gaatgtcaaa ggaagactct gcctggcctt cctgc 45

<210> 8
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 8
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35

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 9
ttcgcgaatg aatgtcaaag gaagactctg

30

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric,
Homo Sapiens and Sus Domesticus

<400> 10
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32

<210> 11
<211> 6
<212> PRT
<213> Sus scrofa

<400> 11
Met Asn Val Lys Gly Arg
1 5

<210> 12
<211> 6
<212> PRT
<213> Mus musculus

<400> 12
Met Asn Val Lys Gly Lys
1 5

<210> 13
<211> 6
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Bovine

<400> 13
Met Val Val Lys Gly Lys
1 5

<210> 14
<211> 6
<212> PRT
<213> Sus scrofa

<400> 14
Met Asn Val Lys Gly Arg
1 5